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IL17RLP Nucleotid and Amino Acid Sequence

1	GCACGAGCGATGTCGCTCGTGTGCTAAGCCTGGCCGCGTGTGCAGGAGGCCGTACCC	60
1	<u>M S L V L L S L A A L C R S A V P</u>	17
61	CGAGAGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAA	120
18	<u>R E P T V Q C G S E T G P S P E W M L Q</u>	37
121	CATGATCTAATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGT	180
38	H D L I P G D L R D L R V E P V T T S V	57
181	GCAACAGGGGACTATTCAATTGGATGAATGTAAGCTGGTACTCCGGCAGATGCCAGC	240
58	A T G D Y S I L M N V S W V L R A D A S	77
	<i>Domain I</i>	
241	ATCCGCTTGTGAAGGCCACCAAGATTGTGTGACGGGCAAAAGCAACTTCCAGTCCTAC	300
78	<u>I R L L K A T K I C V T G K S N F Q S Y</u>	97
	<i>Domain I</i>	
301	AGCTGTGTGAGGTGCAATTACACAGAGGCCCTCCAGACTCAGACCAGACCCCTCTGGTGGT	360
98	S C V R C N Y T E A F Q T Q T R P S <u>G G</u>	117
361	AAATGGACATTTCTACATGGCTTCCCTGTAGAGCTGAACACAGTCTATTCTATTGGG	420
118	<u>K W T F S Y I G F P V E L N T V Y F I G</u>	137
421	GCCCATAATATCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTC	480
138	A H N I P N A N M N E D G P S M S V N F	157
481	ACCTCACCAAGGCTGCCTAGACCACATAATGAAAATAAAAAAAGTGTGTCAAGGCCGA	540
158	T S P G C L D H I M K Y K K K <u>C V K A G</u>	177
	<i>Domain II</i>	
541	AGCCTGTGGGATCCGAACATCACTGCTTGTAAAGAAGAATGAGGAGACAGTAGAAAGTGAAC	600
178	<u>S L W D P N I T A C K K N E E T V E V N</u>	197
	<i>Domain II</i>	
601	TTCAACCACTCCCTGGAAACAGATACTGGCTCTTATCCAACACAGCACTATCATC	660
198	F T T T P L G N R Y M A L I Q H S T I I	217
661	GGGTTTCTCAGGTGTTGAGCCACACCAAGAAAGAACAAACGCGAGCTTCAGTGGTGATT	720
218	G F S <u>Q V F E P H Q K K Q T R A S V V I</u>	237
	<i>Domain III</i>	

FIG. 1A

IL17RLP Nucleotide and Amino Acid Sequence

721	CCACTGACTGGGATAGTGAAGGTGCTACGGTCAGCTGACTCCATATTTCCTACTTGT	780
238	P V T G D S E G A T V Q L T P Y F P T C	257
781	GGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCAACAAACAGGCGTCCCT	840
258	G S D C I R H K G T V V L C P Q T G V P <i>Domain IV</i>	277
841	TTCCCTCTGGATAACAACAAAGCAAGCCGGAGGCTGGCTGCCTCTCCTCCTGCTGTCT	900
278	F P L D N N K S K P G G W L P L L L L S <i>Domain V</i>	297
901	CTGCTGGTGGCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGG	960
298	L L V A T W V L V A G I Y L M W R H E R	317
961	ATCAAGAAGACTTCCTTTCTACCACACACTACTGCCCCCATTAAGGTTCTTGTGGTT	1020
318	I K K T S F S T T T L L P P I K V L V V <i>Domain VI</i>	337
1021	TACCCATCTGAAATATGTTCCATCACACAATTGTTACTTCACTGAATTCTTCAAAC	1080
338	X P S E I C F H H T I C Y F T E F L Q N <i>Domain VI</i>	357
1081	CATTGCAGAAGTGAGGTCACTCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGT	1140
358	H C R S E V I L E K W Q K K K I A E M G <i>Domain VII</i>	377
1141	CCAGTGCAGTGGCTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTCCTTCTTCC	1200
378	P V Q W L A T Q K K A A D K V V F L L S	397
1201	AATGACGTCAACAGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAG	1260
398	N D V N S V C D G T C G K S E G S P S E	417
1261	AACTCTCAAGACTCTCCCTTGCTTAACCTTCTGCAGTGATCTAAGAAGCCAGAT	1320
418	N S Q D S S P C L	426
1321	TCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAGACGATTACAA	1380
1381	TGCTCTCAGTGTCTGCCCAAGTACCAACCTCATGAAGGATGCCACTGCTTCTGTGCAGA	1440
1441	ACTTCTCCATGTCAAGTAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGG	1500

FIG. 1B

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IL17RLP Nucleotide and Amino Acid Sequence

1501	CTGCTGCTCCTTGTAGCCCACCCATGAGAAGCAAGWGACCTAAAGGCTTCTATCCCAC	1560
1561	CAATTACAGGGAAAAACGTGTGATGATCCTGAAGCTTACTATGCAGCCTACAAACAGCC	1620
1621	TTAGTAATTAAAACATTTATACCAATAAAATTTCAAATATTGCTAACTAATGTAGCAT	1680
1681	TAACTAACGATTGGAAACTACATTTACAACCTCAAAGCTGTTTATACATAGAAATCAAT	1740
1741	TACAGTTTAAATTGAAAATTAACCATTGATAATGCAACAATAAGCATCTTCAGCC	1800
1801	AAAAAAAAAAAAAAA 1816	

FIG. 1C

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IL17RLP vs. murin IL17R

Percent Similarity: 49.879 Percent Identity: 28.571

IL17RLP.aa
x
mIL17R.aa

1	MSLVLLSLAALCRS.AVPRE...PTVQCGSE.....	TGPSPEWMLQ	37
16	LGWLWLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHP		65
38	HDLIPGDLRDLRVEPVTTSVATGDYSILMNVSWVLRADASIRLLKATKIC		87
66	KNLTPSSPKNIYINILSVSSTQHGELEVPLHVEWTLQTDASILYLEGAELS		115
88	VTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIG		137
116	VLQLNTNERL.CVKFQFLSMLQHHRK...RWRFSFSHFVVDPGQEYEV		160
138	AHNIPNANMNEGPMNSVNFSPGCLDHIMKYKKKCVKAGSLWDPNITAC		187
161	VHHLPKPIPDPGDPNHKSIIIFVPCEDSKMKMTTSCVSSGSLWDPNITVE		210
188	KKNEETVEVNFTTPLGNRYMALIQ.....HSTIIGFSQVFEPHQKK		229
211	TLDTQHLRVDFTLWNESTPYQLLESFSDSENHSCFDVVKQIFAPRQEEF		260
230	QTRASVVIPVTGD..SEGATVQLTPYFPTCGSDCIRHKGT	V..VLCPQTG	275
261	HQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTT		310
276	VPFPLDNNKSKPGGWLPPLL.....LLSLLVATWVLVAGIYLMWRHERIK		319
311	VPKPV.....ADYIPLWVYGLITLIAILLVGSVIVLIIICMTWRLSGAD		353
320	KTSFS.....TTTLLPPIKVLVVYPSEICFHHTICY.FTEF		354
354	QEKGDDSKINGILPVADLTPPPLRPRKWIVYSAHDPLYVEVVLKFAQF		403
355	LQNHCRCSEVILEKWQKKKIAEMGPVQWLATOKK....AADKVVFLLSNDV		400
404	LITACGTEVALDLLEEQQVISEVGVMTWVSRQKQEMVESNSKIIIILCSRGT		453
401	NSVCDGTCGKSEGSPSENSQDSSPC		425
454	QAKWKAILGWAEPAVQLRCDHWKPA		478

FIG. 2

IL17RLP Protein Analysis

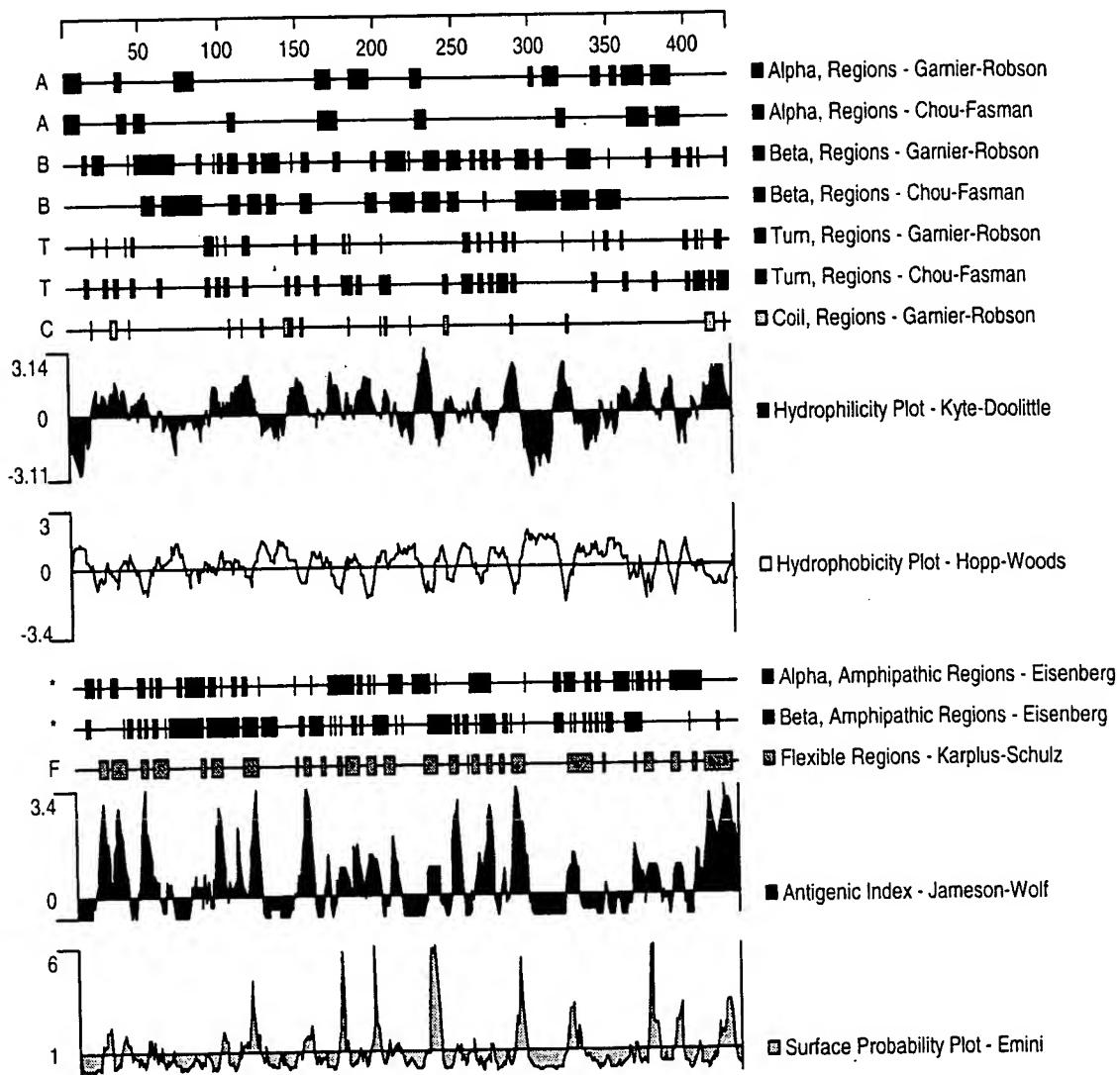


FIG. 3